



SEQUENCE LISTING

<110> Chan, Lia Raquel
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Gago, Gabriela Marisa
Dunan, Claudio Marcelo

<120> Transcription Factor Gene Induced by Water Deficit Conditions and
Absciscic Acid from Helianthus Annuus, Promoter and Transgenic Plants

<130> 2510.0040000/JAG/SAC

<140> 10/520,333

<141> 2003-05-02

<150> PCT/US2003/013770

<151> 2003-05-02

<160> 30

<170> PatentIn version 3.1

<210> 1

<211> 774

<212> DNA

<213> Helianthus annuus

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gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat	300
aacgcgctaa agcataacta cgagacgctt gcgtctaat ccgagtctct aaagaaagag	360
aatcaggccc tactcaatca ggtatggttg caaacttaca atgttgcatt caactattta	420
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agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtggca	540
gcggtgaaga atcggtgat cggtttacga actctccgga cgttatgttt ggtcaagaaa	600
tgaatgttcc gttttgacac ggttttgcgt actttgaaga aggaaacagt ttgttggaga	660
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 cccgagttta ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg 240
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 ggaaacagtt tggtggagat tgaagaacaa ctgccagacc ctcaaaagtg gtgggagttc 600
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<210> 3
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 <213> Helianthus annuus

<220>
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 <222> (1)..(1221)
 <223> Large allele

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<210> 4
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 <213> Artificial Sequence

<220>
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 II site

<400> 4	
gcgaagcttg atgcgaacga gtggttta	28

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 5	
gcggtcgaca cctggcacat cgtatctt	28

<210> 6
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Bam HI site

 <400> 6
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 <210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Hind I II site

 <400> 7
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 <210> 8
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 <220>
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 <400> 8
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 <210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the 5' promoter

 <400> 9
 atttcgcaag tagtccatt 19

 <210> 10
 <211> 1015
 <212> DNA
 <213> Helianthus annuus

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gattcttgct aaattcaacg cgtacacctg tgcttcatct aaaccata ctttaagaac 960
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<210> 11
<211> 28
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<220>
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<400> 11
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<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> Designed oligonucleotide for cloning 5' cDNA and having Bam HI s
ite

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<400> 12
ggcggatccc ctggtggttg tttctgttg 29

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<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide based on 5' cDNA and having Xho I site

 <400> 13
 gaggactcga gctcaagttt tttttttttt tttt 34

 <210> 14
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide based on 5' cDNA and having Xho I site

 <400> 14
 gaggactcga gctcaagc 18

 <210> 15
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter and having Eco RI
 site

 <400> 15
 gccgaattca gattgagcaa gagtataac 29

 <210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide based on the promoter

 <400> 16
 acctttataa agaccactc 19

 <210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence
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 <223> Designed oligonucleotide based on the promoter

<400> 17
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<210> 18
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 18
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<210> 19
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 <212> DNA
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<220>
 <223> oligonucleotide to DNA-binding assays

<400> 19
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<210> 20
 <211> 30
 <212> DNA
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<220>
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<400> 20
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<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide having Sac I site

<400> 21
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<210> 22
 <211> 27
 <212> DNA
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<220>
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<400> 22
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27

7

<210> 23
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<212> DNA
<213> Helianthus annuus

<220>
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<222> (5)..(5)
<223> n is a or t

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9

<210> 24
<211> 181
<212> PRT
<213> Helianthus annuus

<400> 24

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Arg Asn Glu Gly Arg Lys Arg Phe Thr Asp Lys Gln Ile Ser Phe Leu
20 25 30

Glu Tyr Met Phe Glu Thr Gln Ser Arg Pro Glu Leu Arg Met Lys His
35 40 45

Gln Leu Ala His Lys Leu Gly Leu His Pro Arg Gln Val Ala Ile Trp
50 55 60

Phe Gln Asn Lys Arg Ala Arg Ser Lys Ser Arg Gln Ile Glu Gln Glu
65 70 75 80

Tyr Asn Ala Leu Lys His Asn Tyr Glu Thr Leu Ala Ser Lys Ser Glu
85 90 95

Ser Leu Lys Lys Glu Asn Gln Ala Leu Leu Asn Gln Leu Glu Val Leu

100	105	110
Arg Asn Val Ala Glu Lys His Gln Glu Lys Thr Ser Ser Ser Gly Ser		
115	120	125
Gly Glu Glu Ser Asp Asp Arg Phe Thr Asn Ser Pro Asp Val Met Phe		
130	135	140
Gly Gln Glu Met Asn Val Pro Phe Cys Asp Gly Phe Ala Tyr Phe Glu		
145	150	155
Glu Gly Asn Ser Leu Leu Glu Ile Glu Glu Gln Leu Pro Asp Pro Gln		
	165	170
Lys Trp Trp Glu Phe		
180		
<210> 25		
<211> 99		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Synthetic Hd-Zip domain of Athb-1		
<400> 25		
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Glu Lys Ser Phe Glu Thr Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr		
20	25	30
Gln Leu Ala Lys Lys Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp		
35	40	45
Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Arg Asp		
50	55	60
Tyr Asp Leu Leu Lys Ser Thr Tyr Asp Gln Leu Leu Ser Asn Tyr Asp		
65	70	75
Ser Ile Val Met Asp Asn Asp Lys Leu Arg Ser Glu Val Thr Ser Leu		
85	90	95

Thr Glu Lys

<210> 26
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Hd-Zip domain of Athb-6

<400> 26

Leu Ser Glu Lys Lys Arg Arg Leu Ser Ile Asn Gln Val Lys Ala Leu
1 5 10 15

Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Val
20 25 30

Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp
35 40 45

Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp
50 55 60

Tyr Gly Val Leu Lys Thr Gln Tyr Asp Ser Leu Arg His Asn Phe Asp
65 70 75 80

Ser Leu Arg Arg Asp Asn Glu Ser Leu Leu Gln Glu Ile Ser Lys Leu
85 90 95

Lys Thr Lys

<210> 27
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Hd-Zip domain of Athb-7

<400> 27

Asn Lys Asn Asn Gln Arg Arg Phe Ser Asp Glu Gln Ile Lys Ser Leu
1 5 10 15

Glu Met Met Phe Glu Ser Glu Thr Arg Leu Glu Pro Arg Lys Lys Val

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Gln	Leu	Ala	Arg	Glu	Leu	Gly	Leu	Gln	Pro	Arg	Gln	Val	Ala	Ile	Trp
	35				40				45						
Phe	Gln	Asn	Lys	Arg	Ala	Arg	Trp	Lys	Ser	Lys	Gln	Leu	Glu	Thr	Glu
	50				55						60				
Tyr	Asn	Ile	Leu	Arg	Gln	Asn	Tyr	Asp	Asn	Leu	Ala	Ser	Gln	Phe	Glu
65				70					75						80
Ser	Leu	Lys	Lys	Glu	Lys	Gln	Ala	Leu	Val	Ser	Glu	Leu	Gln	Arg	Leu
				85					90					95	

Lys Glu Ala

<210> 28
 <211> 99
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic Hd-Zip domain of Athb-12
 <400> 28

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			20					25					30		
Gln	Val	Ala	Arg	Glu	Leu	Gly	Leu	Gln	Pro	Arg	Gln	Met	Thr	Ile	Trp
	35					40					45				
Phe	Gln	Asn	Lys	Arg	Ala	Arg	Trp	Lys	Thr	Lys	Gln	Leu	Glu	Lys	Glu
	50					55					60				
Tyr	Asn	Thr	Leu	Arg	Ala	Asn	Tyr	Asn	Asn	Leu	Ala	Ser	Gln	Phe	Glu
65				70					75						80
Ile	Met	Lys	Lys	Glu	Lys	Gln	Ser	Leu	Val	Ser	Glu	Leu	Gln	Arg	Leu
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Asn Glu Glu

<210> 29
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Hd-Zip domain of Hahb-4

<400> 29

Arg Asn Glu Gly Arg Lys Arg Phe Thr Asp Lys Gln Ile Ser Phe Leu
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Glu Tyr Met Phe Glu Thr Gln Ser Arg Pro Glu Leu Arg Met Lys His
20 25 30

Gln Leu Ala His Lys Leu Gly Leu His Pro Arg Gln Val Ala Ile Trp
35 40 45

Phe Gln Asn Lys Arg Ala Arg Ser Lys Ser Arg Gln Ile Glu Gln Glu
50 55 60

Tyr Asn Ala Leu Lys His Asn Tyr Glu Thr Leu Ala Ser Lys Ser Glu
65 70 75 80

Ser Leu Lys Lys Glu Asn Gln Ala Leu Leu Asn Gln Leu Glu Val Leu
85 90 95

Arg Asn Val

<210> 30
<211> 66
<212> PRT
<213> Artificial Sequence

<220> 30
<223> Synthetic fragment of Hahb-4

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Ser Asp Asp Arg Phe Thr Asn Ser Pro Asp Val Met Phe Gly Gln Glu
20 25 30

Met Asn Val Pro Phe Cys Asp Gly Phe Ala Tyr Phe Glu Glu Gly Asn
35 40 45

Ser Leu Leu Glu Ile Glu Glu Gln Leu Pro Asp Pro Gln Lys Trp Trp
50 55 60

Glu Phe
65